

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 26, 2002, 21:05:13 ; Search time 11 Seconds

Post-processing: Minimum Match 0%

Database : Swissprot_40; *

Title: Perfect score: US-09-840-795-19
Sequence: 1 MDQQENEYWDQWRCVTCQR.....AQQLFSLSDLSDVP1PQQQQGPEM 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153.5	12.1	260	1 TNR7_HUMAN	P26842 homo sapien
2	152.0	415	1	TNR3_MOUSE	P50284 mus musculus
3	145.5	11.4	455	1 TRIA_HUMAN	P19438 homo sapien
4	145	11.4	454	1 TRIA_MOUSE	P23118 mus musculus
5	143.5	11.3	500	1 TNR7_MOUSE	P41272 mus musculus
6	143	11.2	332	1 TNR6_PIG	07735 sus scrofa
7	142	11.2	625	1 TRI1_MOUSE	033305 mus musculus
8	141.5	11.1	283	1 TRI4_HUMAN	092956 homo sapien
9	134.5	10.6	323	1 TNR6_BOVIN	P51867 bos taurus
10	134.5	10.6	461	1 TRIA_PIG	P50555 sus scrofa
11	134	10.6	471	1 TRIA_BOVIN	019131 bos taurus
12	134	10.5	435	1 TNR3_HUMAN	P31941 homo sapien
13	132.5	10.4	461	1 TRIB_HUMAN	P24333 homo sapien
14	130	10.2	461	1 TRIA_RAT	P22934 rattus norvegicus
15	129.5	10.2	255	1 TNR9_MOUSE	P20334 mus musculus
16	129.5	10.2	327	1 TNR6_MOUSE	P22446 mus musculus
17	124.5	9.8	255	1 TNR9_HUMAN	007011 homo sapiens
18	124	9.7	616	1 TR11_HUMAN	Q96696 homo sapien
19	122	9.6	1006	1 EPB6_HUMAN	01197 human
20	121	9.5	324	1 TNR6_RAT	063199 rattus norvegicus
21	119	9.3	335	1 TNR6_HUMAN	P2445 homo sapien
22	118	9.3	474	1 TRIB_MOUSE	P22119 mus musculus
23	117	9.2	471	1 TR12_HUMAN	Q93038 Homo sapiens
24	116.5	9.2	416	1 TR16_CHICK	P15159 gallus gallus
25	114.5	9.0	271	1 TNR4_RAT	P15725 rattus norvegicus
26	114	9.0	326	1 VT2_MXVIL	P22825 myxoma virus
27	111	8.7	272	1 TNR4_MOUSE	P47741 mus musculus
28	110.5	8.7	1639	1 LMG1_DRONE	P1215 drosophila
29	108	8.5	814	1 AD15_HUMAN	Q14444 homo sapiens
30	108	8.5	1877	1 PCK5_MOUSE	Q04592 mus musculus
31	107.5	8.4	269	1 TNR5_BOVIN	Q28203 bos taurus
32	107	8.4	2569	1 LMA3_MOUSE	Q61789 mus musculus
33	8.4	8.4	1	T10B_HUMAN	DR PRODOM; PD000771; TNFR_c6; 1.
34					PIR; A46454; A46454.
35					DR PIR; A46517.
36					DR HSP; P19438; 1TNR.
37					DR MM; 18671.
38					DR InterPro; IPRO01368; TNFR_c6.
39					DR Pfmf; PFM0020; TNFR_c6; 2.
40					DR PIR; A46454; A46454.
41					DR PIR; A46517.
42					DR HSP; P19438; 1TNR.
43					DR MM; 18671.
44					DR InterPro; IPRO01368; TNFR_c6.
45					DR Pfmf; PFM0020; TNFR_c6; 1.

ALIGNMENTS

008644 mus musculus
09n115 brachioosto
Q2n295 canis familiaris
015230 homo sapiens
061001 mus musculus
P07174 rattus norvegicus
P34015 variola virus
P19137 mus musculus
P25941 homo sapiens
P28089 homo sapiens
P23391 homo sapiens
P14389 homo sapiens

DR	SMART; SW00208; TNFR_2;	DR	Genomics 30:312-319(1995).
PROSITE; PS00652; TNFR_NGFR_1;	PROSITE; PS00652; TNFR_NGFR_1;	CC	-!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
PS0050; TNFR_NGFR_2;	IMMUNE DEVELOPMENT.	CC	-!- IMMUNE DEVELOPMENT.
T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;	T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;	CC	-!- T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW	Phosphorylation.	CC	-!- SUBCELLULAR LOCATION: TYPE I membrane protein.
FT	SIGNAL	CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
FT	CHAIN	CC	-----
FT	21	20	POTENTIAL.
FT	260		TUMOR NECROSIS FACTOR RECEPTOR
FT	DOMAIN	CC	SUPERFAMILY MEMBER 7.
FT	21	191	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	CC	POTENTIAL.
FT	192	212	CYTOSOLIC (POTENTIAL).
FT	DOMAIN	CC	-----
FT	213	260	-----
FT	REPEAT	CC	-----
FT	63	63	-----
FT	REPEAT	CC	-----
FT	104	104	TNFR-CYS 1.
FT	105	141	TNFR-CYS 2.
FT	95	95	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	CC	PHOSPHORYLATION (POTENTIAL).
FT	219	219	-----
FT	CONFFLICT	CC	PHOSPHORYLATION (POTENTIAL).
FT	59	59	A -> T (IN REF. 2).
FT	SEQUENCE	CC	-----
SQ	260 AA;	18;	260 AA;
Query	Match	12.1%	Score 153.5; DB 1; Length 260;
Best Local Similarity	25.9%	Pred. No. 2e-06;	Matches 72; Conservative 29; Mismatches 78; Indels 99; Gaps 18;
Matches	72;		
Conservative	29;		
Mismatches	78;		
Indels	99;		
Gaps	18;		
QY	3 COENYWDQMGRCVTCQRCGPQGELSKDQCGEGDAYCTACPPRKYKSSWGH--KCQ	59	-----
Db	27 CPERHYWAQKLC-CQMCPEGTEVKDCQHRKA-AQCDPCIP-GVFSFPDHHTPHCE	82	-----
QY	60 SCITC--ATYINRQVKVNCCATSNAVCG---DCLPRFRKRTRGGLOPECIPTK-QT	111	-----
Db	83 SCRHHNSGGLVR---NCITANAECACRNGWQC-----RODECTEDDPLPN	125	-----
QY	112 PTSEVQCAFQLS-----LVEA-----DAPTV---PPQEAA	137	-----
Db	126 PSLTARSSQALSPHPOPTHLVYSEMLEARTAGHMOTLADFROLPARTLTHWPQPSRLC	185	-----
QY	138 -----TLVAVVSSLWFLFLAFGLFLGFLYCKQFNRRHCCRQGLLQFEADKTAKEESLFPV	192	-----
Db	186 SDDFTIRILVIFSGMFLVETLA-GALEFLHQRKY-----RSNKGES--PV	226	-----
QY	193 PPKSETARSQVSQVAPGSTAQOLFSDLSVTPQQQOGPE	230	-----
Db	227 EPA-EPCRSQCPREEGS-----TPIQEDYRKPE	255	-----
RESULT	2		
TNFR3_MOUSE	STANDARD;	PRT;	415 AA.
ID	TNFR3_MOUSE		
AC	P0284;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Lymphotxin beta receptor precursor.		
GN	LTBR OR TNFCR OR TNFRSF3.		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TAXID=10990;		
[1]			
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CVB; TISSUE=Lung;		
RX	MEDLINE=96072804; PubMed=7594541;		
RA	Brown W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,		
RA	Hession C., Tizard R., Kozak C.A.,		
RA	"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression.", J. Immunol. 155:5280-5288(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96163885; PubMed=8586432;		
RA	Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,		
RA	Honjo T.; "The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping".		

RESULT 3

TRIA_HUMAN	STANDARD;	PRT;	455 AA.
ID TRIA_HUMAN			
AC P19438;			
DT 01-FEB-1991 (Rel. 17, Created)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Tumor necrosis factor receptor 1 precursor (Tumor necrosis factor binding protein 1) (TNF _P) (p60) (TNF-R1) (p55) (CD120A).			
GN TNFRSF1A OR TNFR1 OR TNFAR.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX NCBI_TAXID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Placenta;			
RX MEDLINE=90235285; PubMed=21598863;			
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,			
RA Gettanaga T., Granger G.A., Lenz R., Raab H., Kohr W.J., Goeddel D.V.,			
RT "Molecular cloning and expression of a receptor for human tumor necrosis factor."			
RT Cell 61:361-370(1990).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=90235284; PubMed=2158862;			
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,			
RA Tabuchi H., Lesslauer W.:			
RT "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor."			
RL Cell 61:351-359(1990).			
RN [3]			
RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RX MEDLINE=9106021; PubMed=1696110;			
RA Nophiar Y., Kempf O., Brakelsch C., Engelmann H., Zwang R.,			
RA Adenka D., Holtmann H., Wallach D.,			
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor."			
RT EMBO J. 9:3269-3278(1990).			
RN			
RP SEQUENCE FROM N.A.			
RX MEDLINE=9109041; PubMed=1702293;			
RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,			
RA Lantz M., Olson T., Hauptmann R., Stritova C., Adolf G.R.,			
RT "Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein."			
RT DNA Cell Biol. 9:705-715(1990).			
RN [5]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Placenta;			
RX MEDLINE=91017509; PubMed=2170974;			
RA Gray P.W., Barrett K., Chanty D., Turner M., Feldman M., Ambros P.F.,			
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein."			
RT Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).			
RN [6]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=92250049; PubMed=1315717;			
RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.,			
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 12p13."			
RT Genomics 13:219-224(1992).			
RN [7]			
RP SEQUENCE OF 41-45.			
RX MEDLINE=90110215; PubMed=2153136;			
RA Engelman H., Novick D., Wallach D.,			
RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors."			

J. Biol. Chem. 265:1531-1536(1990).

RJ [8]

RN X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.

RX MEDLINE=9225869; PubMed=8387091;

RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J., Broger C., Loetscher H., Lesslauer W., "Crystal structure of the soluble human 55 kd TNF receptor-human TNF factor complex: implications for TNF receptor activation." *Nature* 397:431-445(1993).

RJ [9]

RX X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.

RJ MEDLINE=9094982; PubMed=8939750;

RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R., "Structures of the extracellular domain of the type I tumor necrosis factor receptor," *Science* 271:1251-1262(1996).

RJ STRUCTURE 4:1251-1262(1996).

RJ CC RECRUITS: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD OF THE ACTD SPHINGOMYELINASE.

CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (APOTHESE-SPECIFIC CSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYCLOTIDAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF NF-KAPPA B SIGNALING.

CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.

CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.

CC -!- DOMAIN: THE DOMAIN THAT INDUCES A SMASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry; WWW="HTTP://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".

CC -----

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CC -----

DR EMBL: X55313; CAA39021.1; -.

DR EMBL: M33294; AAA03210.1; -.

DR EMBL: M52286; AAA36753.1; -.

DR EMBL: M63121; AAA36754.1; -.

DR EMBL: M73866; AAA61201.1; -.

DR EMBL: M75864; AAA61201.1; JOINED.

DR EMBL: M75865; AAA61201.1; JOINED.

DR EMBL: M60275; AAA36756.1; -.

DR EMBL: A21522; CAA01558.1; -.

DR PIR: A3489; GOHUTL.

DR PIR: A35010; A35010.

DR PIR: S12057; S12057.

DR PIR: A38208; A38208.

DR PIR: 1TNR; 31-JUL-94.

DR PDB: 1NCF; 07-DEC-95.

DR PDB: 1EXT; 11-JAN-97.

DR MIM: 191190; -.

DR InterPro; IPR00488; Death.

DR InterPro; IPR001368; TNFR_C6.

DR Pfam; PF00531; death.

DR Pfam; PF00220; TNFR_C6; 4.

DR Pfdom; PD00071; TNFR_C6; 1.

DR SMART; SM00208; TNFR; 4.

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CC EMBL; M60468; AAA39751.1; --

CC EMBL; M59377; AAA40464.1; --

CC EMBL; X59238; CAA41922.1; --

CC EMBL; X57796; CAA40936.1; --

CC EMBL; L26349; AAQ59361.1; --

CC EMBL; M76656; AAQ40465.1; --

CC EMBL; M88067; AAQ40465.1; JOINED.

DR PIR; A38634; QMSTI.

DR PIR; S19021; S19021.

DR HSSP; P19438; IEXT.

DR PIR; S16677; S16677.

DR SMART; SM00005; DEATH; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.

DR PROSITE; PS00520; TNFR_c6; 1.

DR SMART; SM00028; TNFR; 3.

DR PROSITE; PS00510; TNFR_NGFR_2; 3.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.

FT SIGNAL 1 21

FT CHAIN 22 454

FT DOMAIN 22 212

FT TRANSMEM 213 235

FT DOMAIN 236 454

FT REPEAT 43 82

FT REPEAT 83 125

FT REPEAT 126 165

FT REPEAT 167 196

FT DOMAIN 339 349

FT DOMAIN 356 441

FT DISULFID 44 58

FT DISULFID 59 72

FT DISULFID 62 81

FT DISULFID 84 99

FT DISULFID 102 117

FT DISULFID 105 125

FT DISULFID 127 143

FT DISULFID 146 158

FT DISULFID 149 166

FT DISULFID 168 179

FT DISULFID 182 191

FT DISULFID 185 195

FT CARBOHD 151 154

FT CARBOHYD 151 154

FT CARBOHD 202 202

FT CONFLICT 394 394

SO SEQUENCE 454 AA; 50129 MW; 07102C2E8C3C2B6D9 CRC64;

Query Match 11.4%; Score 145; DB 1; Length 454; Best Local Similarity 21.9%; Pred. No. 1.9e-05; Matches 67; Conservative 37; Mismatches 112; Indels 90; Gaps 14;

Oy 3 COENEYNDQWGRCVTCTCORGPGOELSKDCGYEGGDAVCTACPPRKYKSWGH-HKCSC 61

Oy 44 CPQGKVYHVKNNISNICRKCKHGKVLYSDCC-SPGRDRTVORECGKTFTASQNLRLQCSC 102

Db 62 ITC-AVINRVRKVNTATSAVCG-----DCLPRFRKTRI-----96

Db 103 KTCRKEMSEVEISPQCDKDVTCGCKENQFQLSETHEFOCVCSPCFNGTVWIPCKETQ 162

Qy 97 -----GG---LQDQECLPTCTQPTPSBVQCAFOLSLIVADAPTVPPOEATVALVSSL 147

RESULT 5 TNR7_MOUSE ID TNR7_MOUSE STANDARD; PRT; 250 AA.

AC P41272;

DR 01-FEB-1995 (Rel. 31, Created)

DR 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 7 precursor (CD27L receptor) (T-cell activation antigen CD27).

GN TNFRSF7 OR CD27.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI-TaxID=10090; RN [1]-SEQUENCE FROM N_A.

RC STRAIN=B6CBA; TISSUE=Thymus;

RX MEDLINE=93120926; PUBMED=838462;

RA Gravesteen L.A., Blom B., Nolten L.A., de Vries E., van der Horst G., RA Ossendorp F., Borst J., Loenen W.A.;

RT "Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte-specific member of the nerve growth factor receptor family"; RT Eur. J. Immunol. 23:943-950(1993).

RT -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.

CC -!- TISSUE SPECIFICITY: IN THYMUS AND SPLEEN, BUT NOT IN NON-LYMPHOID TISSUES.

CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.

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CC EMBL; L24495; -; NOT_ANNOTATED_CDS.

DR PIR; A49033; A49053.

DR HSSP; P19438; IINC.

DR MGD; MGI:088326; Tnfrsf7.

DR InterPro; IPR001368; Tnfr_c6.

DR Pfam; PF00020; TNFR_c6; 2.

DR ProDom; P000071; TNFR_c6; 1.

DR SMART; SM00028; TNFR; 2.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00520; TNFR_NGFR_2; 1.

DR T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat; SIGNAL 1 20

FT CHAIN 21 250

FT TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 7.

FT EXTRACELLULAR (POTENTIAL).

FT CYTOPLASMIC (POTENTIAL).

Db 200 A-----EQVSWAPGLAQF-----SLDSVP 221

Db 277 GFNPTLGFSTPGFSSPVSSP--ISPIFGPSNWHEMPVSEVVPTQGADPLLYESLCSP 334

Qy 222 IPQQQ 227

Db 335 APTSVQ 340

FT REPEAT 26 63 TNFR-CYS 1.
 FT REPEAT 64 104 TNFR-CYS 2.
 FT REPEAT 105 141 TNFR-CYS 3.
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 250 AA; 28164 MW; 48477C2E0C244697 CRC64;

Query Match 11.3%; Score 143.5; DB 1; Length 250;
 Best Local Similarity 25.7%; Pred. No. 1.4e-05;
 Matches 67; Conservative 22; Mismatches 97; Indels 75; Gaps 14;

QY 3 COFNEWYDQWGRGVTQRCGPGQELS RDCKCGEGGDAYCTACPPRKYKSSWGHK--CQS 60
 Db 27 CPDKHWTGGIC--CRMCRGCFVFKDCEQDRTA-AQCDPCIPGTFSFSPDYHTRPHCES 83
 QY 61 CTCAVINRQVNQVNTSNAVCGDCLPRFRKTRIGLQDGECIPCTKTPPTSVQCAF 120
 Db 84 CRHCNSNGLIR--NCVTVANAECC--SSSKNNW--CRODECBC--DPPLNPALTR 130
 QY 121 QLSLVEADAPVPP-----QEAATLVNLSS--LLVFT 151
 Db 131 QPS--ETPSPOPPPTPHGTEPKPSWPLHQLPNSTVYSGRSSRHPCLSSDCIRIVTFS 188
 QY 152 LAFLGILFLFLYCKQQFFRHQRCGQGLQFEADTKAKERSLFP--VPPSKETSAESQVSWAPG 209
 Db 189 SMFL--IFVLGAIFFQRNRHGP---NEDRQAVPEEPCPYSCPREEGSA---- 234
 QY 210 SLAQLFSDLSPVPIPOOQGP 230
 Db 235 -----IPIQEDYRKPE 245

RESULT 6
 TNR6_PIG STANDARD; PRT; 332 AA.

ID TNR6_PIG STANDARD; PRT; 332 AA.
 AC 077736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Receptor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
 DE TNFRSF6 OR APT1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartioactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]

SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT "Expression of apoptosis-associated genes in hibernating and stunned myocardium of pig;"
 RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RECEPTOR FOR A CYTOINE LIGAND KNOWN AS FASL. THE ADAPTER MOLECULE FADD RECRUTS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVATED CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATIC-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 -!- SUBCELLULAR LOCATION: Type I membrane protein.
 -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTER PROTEINS.
 -!- SIMILARITY: CONTAINS 3 TNPW-CYS REPEATS.

-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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 CC or
 CC ---
 DR EMBL; AJ001202; CAA04596; 1; -.
 DR HSSP; P2545; IDDF.
 DR InterPro; IPR00488; Death.
 DR InterPro; IPR01368; TNFR_C6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2.
 DR PROSITE; PS5007; DEATH_DOMAIN; 1.
 DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 16 TUMOR NECROSIS FACTOR RECEPTOR
 FT CHAIN 17 332
 FT DOMAIN 17 175 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 176 192 POTENTIAL.
 FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 45 81 TNFR-CYS 1.
 FT REPEAT 82 125 TNFR-CYS 2.
 FT REPEAT 126 164 TNFR-CYS 3.
 FT DOMAIN 227 311 DEATH.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 TNFR-CYS 4.
 SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;

Query Match 11.2%; Score 143; DB 1; Length 332;
 Best Local Similarity 31.2%; Pred. No. 2e-05; 40; Mismatches 15; Indels 20; Gaps 8; Matches 40; Conservative 15; Mismatches 53; Indels 20; Gaps 8;

QY 2 DCQENEWYDQWGRGVTQRCGPGQELS RDCKCGEGGDAYCTACPPRKYKSSWGHK--KQ 59
 Db 45 ECPEQSHRE-GQ-FCCQCPGPKRKHAK-TSGQAPQVCPSEGEDYTDKHNHSSCR 100
 QY 60 SCITCAVINRQVNQVNTSNAVCGDCLPRFRKTRIGLQDGECIPCT-----KQ 110
 Db 101 RCYRVQDGHEGLEVKNCIRTQNKC-RCKPNFCHTS---QCEHCNCTCBBGVENC 155
 QY 111 TPTSEVQC 118
 Db 156 TPTSNTKC 163

RESULT 7
 TR11_MOUSE STANDARD; PRT; 625 AA.

ID TR11_MOUSE STANDARD; PRT; 625 AA.
 AC 03505;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Receptor necrosis factor receptor superfamily member 11A Precursor (Receptor activator of NF-KB) (osteoclast differentiation factor receptor) (OPFR).
 DE TNFRSF11A OR RANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soricomorpha; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=9803297; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teipe M.C., Dubose R.F., Cosman D., Galibert L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RP [2]
 FUNCTION.

RESULT 9

FT DOMAIN	203	223	POTENTIAL_CYS (POTENTIAL).
FT REPEAT	224	203	CYTOPLASMIC (POTENTIAL).
FT REPEAT	42	75	TNFR-CYS 1.
FT REPEAT	78	119	TNFR-CYS 2.
FT DISULFID	121	162	TNFR-CYS 3.
FT DISULFID	42	53	BY SIMILARITY.
FT DISULFID	54	67	BY SIMILARITY.
FT DISULFID	57	75	BY SIMILARITY.
FT DISULFID	78	93	BY SIMILARITY.
FT DISULFID	96	111	BY SIMILARITY.
FT DISULFID	99	119	BY SIMILARITY.
FT DISULFID	121	127	BY SIMILARITY.
FT DISULFID	138	162	BY SIMILARITY.
FT CARBOHYD	110	110	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	173	173	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	17	17	K -> R (IN REF. 1).
SQ SEQUENCE	283 AA;	30392 MW;	46CE13C270242C1 CRC64;

Query Match Best Local Similarity 11.1%; Score 141.5; DB 1; Length 283; Pred. No. 2.3e-05; Mismatches 63; Conservative 25; Indels 53; Gaps 14;

QY 3 CQENEYWDQWGRGCVTCQRCGPQQEISLSDKGYGGDAYCTACPPRKYKSSW-GHMKCOSC 61

Db 42 CKEDELY-PVGSPEC--CPKCPGPGYRVEKEACELTG--TVCBPCPOTYIAMIHLNLSKCLQC 96

QY 62 ITC- AVINRVKVNTATSNAVCGCDCLP-----RFLY----RKTRIGG 98

Db 97 QMCDFPAMGLRASR-NCSRTENAVCG-CSPGHFCITQVDGDHCAACRAYATSSPGQRVQKG 154

QY 99 LQDQE----CIPCKQKTPSEVQAFOLS---VEADATPVPOEATLVAVLVSLLVVF 150

Db 155 TESQDTLCQNCPGTFSPNGTLECOHQTKCSWLVTKAGAGTSSHHWWNNFLSGSLIVI 214

Qy 151 TLAFGLGLEFLYCKQFNRKHQCGGILQF-----EADKTAKESLFFVPPSKETSA 200

Db 215 VCSTVGL--ITC--VKRRKPRGDIVKVTVSVORKRQEAEGEATVIEALQAPPVTTVA 268

RESULT 9

ID TNR6_BOVIN	STANDARD;	PRT;	323 AA.
ID TNR6_BOVIN	STANDARD;	PRT;	323 AA.
AC P51867;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 16-Oct-2001 (Rel. 40, Last annotation update)			
DE Tumor necrosis factor receptor superfamily member 6 precursor (PASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95). OR APT1 OR FAS.			
GN TNFRSF6			
OS Bos taurus (Bovine).			
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Metazoa; Chordiactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.			
OX NCBI_TaxId=9913;			
RP [1] SEQUENCE FROM N.A.			
RX MEDLINE:95226401; PubMed=8634151;			
RA Yoo J., Stone R.T., Beattie C.W.; "Cloning and characterization of the bovine Fas.", DNA Cell Biol. 15:227-234 (1996).			
RT -- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATIC-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).			
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC -!- DOMAIN: Contains a death domain involved in the binding of FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTER PROTEINS.			

RESULT 10

ID TRIA_PIG	STANDARD;	PRT;	461 AA.
ID TRIA_PIG	STANDARD;	PRT;	461 AA.
AC P5055;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 16-Oct-2001 (Rel. 40, Last annotation update)			
DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RI) (p55) TNFSF1A OR TNFR1.			
GN TNFSF1A			
OS Sus scrofa (Pig).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordiactyla; Suina; Suidae; Sus.			
OX NCBI_TaxId=9023;			
RP [1] SEQUENCE FROM N.A.			
RC TISSUE=Kidney;			
RX MEDLINE:96011645; PubMed=7590278;			
RA Suter B., Pauli U.H.; "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.",			
RT			

-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPТОRS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
 -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 EMBL; U19994; AAC48499.1; -.
 HSSP; P19438; ITRN.
 InterPro; IPR00488; Death.
 InterPro; IPR01368; TNFR_C6.
 Pfam; PF00331; death; 1.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR Prodrom; PDO0071; TNFR_C6; 1.
 DR SMART; SM0005; DEATH; 1.
 DR SMC00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL; 1 21 POTENTIAL.
 FT CHAIN; 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN; 22 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 233 POTENTIAL.
 FT DOMAIN; 234 461 CYTOPLASMIC (POTENTIAL).
 FT REPEAT; 43 82 TNFR-CYS 1.
 FT REPEAT; 83 125 TNFR-CYS 2.
 FT REPEAT; 126 166 TNFR-CYS 3.
 FT REPEAT; 167 195 TNFR-CYS 4.
 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN; 340 350 DEATH.
 FT DISUFD; 362 447 BY SIMILARITY.
 FT DISUFD; 447 58 BY SIMILARITY.
 FT DISUFD; 59 72 BY SIMILARITY.
 FT DISUFD; 81 82 BY SIMILARITY.
 FT DISUFD; 84 99 BY SIMILARITY.
 FT DISUFD; 102 117 BY SIMILARITY.
 FT DISUFD; 105 125 BY SIMILARITY.
 FT DISUFD; 127 143 BY SIMILARITY.
 FT DISUFD; 145 158 BY SIMILARITY.
 FT DISUFD; 149 166 BY SIMILARITY.
 FT DISUFD; 168 179 BY SIMILARITY.
 FT DISUFD; 182 190 BY SIMILARITY.
 FT CARBHYD 185 194 BY SIMILARITY.
 FT CARBHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBHYD 145 145 N-LINKED (SICNAc. . .) (POTENTIAL).
 FT CARBHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 461 AA; 50695 MW; CD72361E60C9D3 CRR64;

 QY 3 COQENEWWDQMRQCVTCQRCGPQELSKDCGGEGGDACTACPPRRYKSSMH-HKQSC 61
 Db 44 CPQENEWWDQMRQCVTCQRCGPQELSKDCGGEGGDACTACPPRRYKSSMH-HKQSC 61
 QY 62 ITC-AVINVRQVNRGTTATSNAVCGCQLPREFRK--TRIGLQLODEC-----IPCTKQ 110
 Db 103 SKCRSEMSOVSIEISPCTVDRIVCG-CRKNQQRKYKNSETLFQCLNSLCPCNGTSLCPNQTQVQPLCER 161
 QY 111 TPT-----SEVQCAFQSLVMEADAPVPPQ-----EATLVALVSSLWVFIL 152
 Db 162 QDTICNCHSGFFFLRKECVSCVNCKNADCKNLCPATSETRNDFQDGTGTTVLPVIFFGL 221
 QY 153 A----FLGLFLFLYK--OFFNRICORG-GLLQFLAKDKTAEEKS-----LFPVPSKE 197
 Db 222 CLAFLFVFLGACRKYRKPKLUSIICKSPTVKESEPEPLATAPSRCGPIITFSPIPSFP 281
 QY 198 TSAEQQV-SWAPGSAQFSLD-----SPIPQDQGP 229
 Db 282 TTTPSPVPSPSPISSTFTPCDWNSNIKVTSPPKEIAPPQAGP 325

RESULT 11
 ID TRIA_BOVIN STANDARD; PRT; 471 AA.
 AC 019131;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-Oct-2001 (Rel. 40, Last annotation update)
 DE (p55).
 GN TNFRFIA OR TNFR1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Acta;
 RA Lee E.-K.; Taylor M.J.; Kehrl M.E.;
 RT "Cloning of cDNA encoding bovine tumor necrosis factor-receptor I
 (TNF-RI)." ;
 RL Submitted [FEB-1997] to the EMBL/GenBank/DDBJ databases.

 -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPТОRS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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DR	Pfam; PF00531; death; 1.	OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
DR	Pfam; PF0020; TNFR_c6; 3.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DR	ProDom; PD000771; TNFR_c6; 1.	OX	NCBI_TaxID=9606;
DR	SMART; SN0005; DEATH; 1.	[1]	
DR	SMAP; SM00208; TNFR; 3.	RN	SEQUENCE FROM N.A.
DR	PS00652; TNFR_NGFR_1; 3.	RP	TISSUE=Liver
PROSITE; PS50017; DEATH_DOMAIN; 1.	PS00505; TNFR_NGFR_2; 3.	RX	RX
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.	RA	Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
SIGNAL	1	RT	"Construction and evaluation of a hincDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.";
FT	CHAIN	RT	Genomics 16:214-218(1993).
FT	DOMAIN	RL	[2]
FT	TRANSMEM	RN	
FT	DOMAIN	RP	FUNCTION
FT	471	RX	MEDLINE=4225209; PubMed=8171323;
FT	233	RA	Crowe P.D., van Aarsdale T.L., Walter B.N., Ware C.F., Hession C.,
REPEAT	471	RA	Ehrenfeis B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
FT	471	RT	"A Lymphotoxin-beta-specific receptor.";
REPEAT	471	RL	Science 264:707-710(1994).
FT	DOMAIN	CC	-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
FT	340	CC	IMMUNE DEVELOPMENT.
FT	372	CC	-1- SUBCELLULAR LOCATION: Type I membrane Protein.
DISULFID	44	CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
DISULFID	59	CC	
DISULFID	62	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
DISULFID	84	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
DISULFID	102	CC	the European Bioinformatics Institute. There are no restrictions on its
DISULFID	105	CC	use by non-profit institutions as long as its content is in no way
DISULFID	127	CC	modified and this statement is not removed. Usage by and for commercial
DISULFID	146	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch.)
DISULFID	149	CC	
DISULFID	166	CC	
DISULFID	179	CC	
DISULFID	182	CC	
DISULFID	185	CC	
DISULFID	194	CC	
DISULFID	194	CC	BY SIMILARITY.
CARBHYD	54	CC	BY SIMILARITY.
CARBHYD	145	CC	(POTENTIAL).
CARBHYD	151	CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	471 AA;	SO	
Query Match	10.6%; Score 134.5; DB 1; Length 471;		
Best Local Similarity	24.4%; Pred. No. 0.00016;		
Matches	68; Conservative 26; Mismatches 120; Indels 65; Gaps 15;		
QY	3 COENEYWDOWGRVCYTQRCGGPGQELSKDCGYYEGGDAYCTACPPRRYKSSWH-HKCOSC 61		
Db	44 CPOCKYKINHPONSTICTKCHKGTYLYNDCP-GFGRDTDCRVAGTYTALENHLRCLSC 102		
QY	62 ITCA-VINVKVNTATSNATNAVGDCPLPRFYKRRIGGLQDQCIPC-----TKOPTPS 114		
Db	103 SRCDEMRCVEISPCVVRDTCVCC-CRKNOYRE-YWGTFGRQLNCPLCNGVNTBQ 159		
QY	115 EVQ-----CAFQLSL-----VEADAPTVP-----PQEAIALVASSL 146		
Db	160 ERDOTTICHMGFFLKGAKCISCHCKNKECEKICPPTRSPGTGKSDQBDGTTVILPLV--- 216		
QY	147 LVVF--TIAFLGLFLFLYCK-----QFFNRHCQFGGLQFEADKTAKEESLFPVPP--PS 195		
Db	217 -IVFGCLIASFASTVVLACKYQRNWKPLYSIICGOSTLV---KEGEPEPLLVPAGFNPT 270		
QY	196 KENSAESQSWARPSLAQFLSLS-----SVPIQQQGP 229		
Db	271 TTICFSSTPSSSPVSPIPPVISCDSNFGAVASPSSETAP 309		
RESULT 12			
TNR3_HUMAN	ID TNR3_HUMAN STANDARD: PRT; 435 AA.		
AC	P35941; 01-JUN-1994 (Rel. 2.9, created)		
DT	01-JUN-1994 (Rel. 2.9, last sequence update)		
DT	16-OCT-2001 (Rel. 4.0, Last annotation update)		
DE	Lymphotoxin-beta receptor precursor (tumor necrosis factor receptor 2 related protein), (Tumor necrosis factor C receptor).		
DE	LTBR OR TNFCR OR TNFRSF3.		
OS	Homo sapiens (Human).		
Query Match	10.5%; Score 134; DB 1; Length 435;		
Best Local Similarity	21.9%; Pred. No. 0.00016;		
Matches	65; Conservative 29; Mismatches 109; Indels 94; Gaps 15;		
QY	4 OENEYWDOWGRVCYTQRCGGPGQELSKDCGYYEGGDAYCTACPPRRYKSSWH-HCSCI 62		
Db	46 QEKYYEPQRH-ICCSRCPGTVVSAK-C-SRIRDIVCATCAENSYNBHWYKTCQLCR 102		
QY	63 TCAVINRQKV-NCTATSNAVC-----GDCLPFRYRTRIG-GL 99		

RESULT 13

ID TRIB_HUMAN	STANDARD;	PRT; 461 AA.
AC P20333;		
DT 01-FEB-1991 (Rel. 17, Created)		
DT 01-AUG-1991 (Rel. 19, Last sequence update)		
DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TNFR2) (p80) (TNF-R2) (p75) (CD120B) (Etanercept).		
DE TNFRSF1B OR TNFR.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX NCBL_TaxID=9606;		
RN [1] SEQUENCE FROM N.A. MEDLINE=92060639; PubMed=2160731;		
RX Smith C.A., Davis T., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.; "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.", Science 248:1019-1023(1990).		
RN [2] SEQUENCE FROM N.A. MEDLINE=9104591; PubMed=2172983;		
RX Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.R., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.", Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).		
RN [3] SEQUENCE FROM N.A. MEDLINE=962299145; PubMed=8661109;		
RX Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslić D., Stallard B.J., Goeddel D.V., Desauvage F.J., Brodeur G.M.; "Physical mapping and genomic structure of the human TNFR2 gene.", Genomics 35:94-100(1996).		
RN [4] SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=00349572; Pubmed-2166946;		
RX Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Rinold G.M.; "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.", Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).		
RP SEQUENCE OF 27-31. MEDLINE=9010215; PubMed=2153136;		
RX Engelmann H., Novick D., Wallach D.; "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.", J. Biol. Chem. 265:1531-1536(1990).		
RN [5] SEQUENCE OF 23-40. MEDLINE=91056048; Pubmed=2173696;		
RX MEDLINE=91056048; Pubmed=2173696;		

RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.B., Lesslauer W., Brockhaus M.; "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).

RA [7] CHARACTERIZATION. MEDLINE=93016040; PubMed=1328224;

RA Pennica D., Lam V.T., Meze N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.; "Biochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation."; J. Biol. Chem. 267:21172-21178(1992).

RA [8] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH TRAF2. MEDLINE=992211490; PubMed=10206649;

RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.; "Structural basis for self-association and receptor recognition of human TRAF2"; Nature 398:533-538(1999).

CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-BETA. APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES

CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immunoglobulin FC chain. It binds to TNF-alpha and blocks its interactions with receptors.

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prowww/ed120b.htm"

CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrelinfo.com/".

CC -----

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CC -----

DR EMBL; M32315; AAA59929; 1; -.

DR EMBL; M35837; AAA63362; 1; -.

DR EMBL; U52165; AAC50522; 1; -.

DR EMBL; U52156; AAC50522; 1; JOINED.

DR EMBL; U52157; AAC50522; 1; JOINED.

DR EMBL; U52158; AAC50522; 1; JOINED.

DR EMBL; U52159; AAC50522; 1; JOINED.

DR EMBL; U52160; AAC50522; 1; JOINED.

DR EMBL; U52161; AAC50522; 1; JOINED.

DR EMBL; U52162; AAC50522; 1; JOINED.

DR EMBL; U52163; AAC50522; 1; JOINED.

DR EMBL; U52164; AAC50522; 1; JOINED.

DR EMBL; M55994; AAA36755; 1; -.

DR PIR; A3536; A35356.

DR PIR; A36007; A36007.

DR PIR; A36475; A36475.

DR PIR; B35010; B35010.

DR PIR; A23666; A23666.

DR PDB; ICAG_12-APR-99.

DR MIM; 191191; -.

DR Inter-Pro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR ProDom; PDO00771; TNFR_c6; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS50050; TNFR_NGFR_2; 4.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

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